In the Claims

Please cancel claims 1, 2, 6, 7, 9-19, 22-32, 36, 37, 39-49, 52-77, 81, 82, 84-94, 96-98.

Please amend the following claims as follows:

C1

8. (ONCE AMENDED) A process for identifying one or more bi-allelic markers linked to a bi-allelic genetic characteristic gene in a species of creatures, comprising the acts of:

a) choosing two or more bi-allelic covering markers so that a CL-F region is systematically covered by the two or more covering markers, the CL-F region being a collection of points on a two-dimensional plane, the two-dimensional plane having the two orthogonal dimensions of chromosomal location and least common allele frequency;

b) choosing a statistical linkage test based on allelic association for each covering marker;

c) choosing a sample of individuals for each covering marker ;

d) obtaining genotype data/sample allele frequency data for each covering marker and the sample chosen for each covering marker, and obtaining phenotype status data for the genetic characteristic for each individual in the sample chosen for each covering marker;

e) calculating evidence for linkage between each covering marker and the gene using the statistical linkage test based on allelic association chosen for each covering marker and the genotype data/sample allele frequency data for each covering marker and using the phenotype status data for the genetic characteristic for each individual in the sample chosen for each covering marker obtained in d); and

f) identifying those covering markers as linked to the genetic characteristic gene which show evidence for linkage based on the calculations of e).

C2

20. (TWICE AMENDED) A process as in claim 8, wherein there is a subgroup of the covering markers, and the markers in the subgroup are a majority of the covering markers, and each marker in the subgroup is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

C3

6 21. (ONCE AMENDED) A process as in claim 20, wherein the process comprises the use of a computer program.

C4

11 50. (TWICE AMENDED) A process for obtaining genotype data/sample allele frequency data as in claim 33, wherein there is a subgroup of the covering markers, and the markers in the subgroup are a majority of the covering markers, and each marker in the subgroup is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

12 51. (ONCE AMENDED) A process for obtaining genotype data/sample allele frequency data as in claim 50, wherein the process comprises the use of a computer program.

C5

17 95. (ONCE AMENDED) One or more copies of a set of oligonucleotides as in claim 78, wherein there is a subgroup of the covering markers, and the markers in the subgroup are a majority of the covering markers, and each marker in the subgroup is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

Please add the following new claims:

18 99. (NEW) A process as in claim 1, wherein there is a subgroup of the covering markers, and the markers in the subgroup are a majority of the covering markers, and each marker in the subgroup is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

C6

19 100. (NEW) A process for obtaining genotype data/sample allele frequency data as in claim 34, wherein there is a subgroup of the covering markers, and the markers in the subgroup are a majority of the covering markers, and each marker in the subgroup is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

20 101. (NEW) One or more copies of a set of oligonucleotides as in claim 79, wherein there is a subgroup of the covering markers, and the markers in the subgroup are a majority of the covering markers, and each marker in the subgroup is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.